Search notes / 29=R arginine / Swissprot alignment

CLUSTAL W (1.82) multiple sequence alignment

```
sp|P01555|CHTA_VIBCH        MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
tr|Q77DI6|Q77DI6_9VIRU      MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
tr|Q8VLI6|Q8VLI6_VIBCH      MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQNEYFD
tr|Q8L356|Q8L356_VIBCH      MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
tr|Q8LTG8|Q8LTG8_9VIRU      MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
tr|Q6KE88|Q6KE88_VIBCH      MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
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                            12345678910111213 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29

sp|P01555|CHTA_VIBCH        RGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHST
tr|Q77DI6|Q77DI6_9VIRU      RGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHST
tr|Q8VLI6|Q8VLI6_VIBCH      RGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHST
tr|Q8L356|Q8L356_VIBCH      RGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHST
tr|Q8LTG8|Q8LTG8_9VIRU      RGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHST
tr|Q6KE88|Q6KE88_VIBCH      RGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHST
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sp|P01555|CHTA_VIBCH        YYIYVIATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHF
tr|Q77DI6|Q77DI6_9VIRU      YYIYVIATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHF
tr|Q8VLI6|Q8VLI6_VIBCH      YYIYVIATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHF
tr|Q8L356|Q8L356_VIBCH      YYIYVIATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHF
tr|Q8LTG8|Q8LTG8_9VIRU      YYIYVIATAPNMFNVNDVLGAYRPHPDEQEVSGLGGIPYSQIYGWYRVHF
tr|Q6KE88|Q6KE88_VIBCH      YYIYVIATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHF
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sp|P01555|CHTA_VIBCH        GVLDEQLHRNRGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHH
tr|Q77DI6|Q77DI6_9VIRU      GVLDEQLHRNRGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHH
tr|Q8VLI6|Q8VLI6_VIBCH      GVLDEQLHRNRGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHH
tr|Q8L356|Q8L356_VIBCH      GVLDEQLHRNRGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHH
tr|Q8LTG8|Q8LTG8_9VIRU      GVLDEQLHRNRGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHH
tr|Q6KE88|Q6KE88_VIBCH      GVLDEQLHRNRGYRDRYYSNLNIAPAADGFGLAGFPPEHKTLREDPWIHH
                            **********************:*******:*********:: **:*****

sp|P01555|CHTA_VIBCH        APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr|Q77DI6|Q77DI6_9VIRU      APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr|Q8VLI6|Q8VLI6_VIBCH      APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr|Q8L356|Q8L356_VIBCH      APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr|Q8LTG8|Q8LTG8_9VIRU      APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr|Q6KE88|Q6KE88_VIBCH      PPPGCGNAPRSSMSNTCDEKPQSLGVKFLDEYQSKVKRQIFSGYPSDIDT
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sp|P01555|CHTA_VIBCH        HNRIKDEL
tr|Q77DI6|Q77DI6_9VIRU      HNRIKDEL
tr|Q8VLI6|Q8VLI6_VIBCH      HNRIKDEL
tr|Q8L356|Q8L356_VIBCH      HNRIEDEL
tr|Q8LTG8|Q8LTG8_9VIRU      HNRIKDEL
tr|Q6KE88|Q6KE88_VIBCH      HNRIKDEL
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CLUSTAL W (1.82) multiple sequence alignment


tr|Q57193|Q57193_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
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tr|Q9RP15|Q9RP15_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q7B9N1|Q7B9N1_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKILSYTE
tr|Q56635|Q56635_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKILSYTE
tr|Q8LT25|Q8LT25_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPQNITDLWAEYHNTQIHTLNDKIFSYTE
sp|P01556|CHTB_VIBCH        MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDKIFSYTE
tr|Q77DH7|Q77DH7_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDKIFSYTE
tr|Q8VLC4|Q8VLC4_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q7BCC5|Q7BCC5_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q94M01|Q94M01_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q5Q031|Q5Q031_VIBCH      MIKLKFGVFFIVLLSSAYAHGTPQNITDLCAEDHNTQIHTLNDKIFSYTE
sp|P13811|ELBH_ECOLI        MNKVKFYVLFTALLSSLCAHGAPQSITELCSEYHNTQIYTINDKILSYTE
                            * *:** *:* .****  ***:*:.** * :* *****:*:****:****

tr|Q57193|Q57193_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q8LT24|Q8LT24_9VIRU      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q9RP15|Q9RP15_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIDRMKDTLRIAYLTE
tr|Q7B9N1|Q7B9N1_VIBCH      SLAGNREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q56635|Q56635_VIBCH      SLAGNREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q8LT25|Q8LT25_9VIRU      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
sp|P01556|CHTB_VIBCH        SLAGKREMAIITFKNGAIFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q77DH7|Q77DH7_9VIRU      SLAGKREMAIITFKNGAIFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q8VLC4|Q8VLC4_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q7BCC5|Q7BCC5_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q94M01|Q94M01_9VIRU      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q5Q031|Q5Q031_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
sp|P13811|ELBH_ECOLI        SMAGKREMVIITFKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTE
                            *:**:***.*****.** ******************:********:****

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tr|Q8LT24|Q8LT24_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
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tr|Q7B9N1|Q7B9N1_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q56635|Q56635_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8LT25|Q8LT25_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
sp|P01556|CHTB_VIBCH        AKVEKLCVWNNKTPHAIAAISMAN
tr|Q77DH7|Q77DH7_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8VLC4|Q8VLC4_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q7BCC5|Q7BCC5_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q94M01|Q94M01_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
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CLUSTAL W (1.82) multiple sequence alignment


tr|Q57193|Q57193_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q8LT24|Q8LT24_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q9RP15|Q9RP15_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q7B9N1|Q7B9N1_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKILSYTE
tr|Q56635|Q56635_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKILSYTE
tr|Q8LT25|Q8LT25_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPQNITDLWAEYHNTQIHTLNDKIFSYTE
sp|P01556|CHTB_VIBCH        MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDKIFSYTE
tr|Q77DH7|Q77DH7_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDKIFSYTE
tr|Q8VLC4|Q8VLC4_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q7BCC5|Q7BCC5_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q94M01|Q94M01_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q5Q031|Q5Q031_VIBCH      MIKLKFGVFFIVLLSSAYAHGTPQNITDLCAEDHNTQIHTLNDKIFSYTE
                            ********** ************:*** * ** *****:******:****

tr|Q57193|Q57193_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
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tr|Q9RP15|Q9RP15_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIDRMKDTLRIAYLTE
tr|Q7B9N1|Q7B9N1_VIBCH      SLAGNREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q56635|Q56635_VIBCH      SLAGNREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q8LT25|Q8LT25_9VIRU      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
sp|P01556|CHTB_VIBCH        SLAGKREMAIITFKNGAIFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q77DH7|Q77DH7_9VIRU      SLAGKREMAIITFKNGAIFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q8VLC4|Q8VLC4_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q7BCC5|Q7BCC5_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q94M01|Q94M01_9VIRU      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
tr|Q5Q031|Q5Q031_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTE
                            ****:************ ******************:**************

tr|Q57193|Q57193_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8LT24|Q8LT24_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q9RP15|Q9RP15_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q7B9N1|Q7B9N1_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q56635|Q56635_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8LT25|Q8LT25_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
sp|P01556|CHTB_VIBCH        AKVEKLCVWNNKTPHAIAAISMAN
tr|Q77DH7|Q77DH7_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8VLC4|Q8VLC4_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q7BCC5|Q7BCC5_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q94M01|Q94M01_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q5Q031|Q5Q031_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
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UniProtKB/Swiss-Prot entry P43529

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**E2BB_ECOLI**
Primary accession number	**P43529**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 32, November 1995
Sequence was last modified in	Release 32, November 1995
Annotations were last modified in	Release 49, January 2006

Name and origin of the protein

Protein name	**Heat-labile enterotoxin IIB, B chain [Precursor]**
Synonym	**LT-IIB**
Gene name	None
From	Escherichia coli [TaxID: 562]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=Isolate 41;
PubMed=2670900 [NCBI, ExPASy, EBI, Israel, Japan]
Pickett C.L., Twiddy E.M., Coker C., Holmes R.K.;
"Cloning, nucleotide sequence, and hybridization studies of the type IIb heat-labile enterotoxin gene of Escherichia coli.";
J. Bacteriol. 171:4945-4952(1989).

[2] X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
DOI=10.1016/S0969-2126(96)00073-1; PubMed=8805549 [NCBI, ExPASy, EBI, Israel, Japan]
van den Akker F., Sarfaty S., Twiddy E.M., Connell T.D., Holmes R.K., Hol W.G.J.;
"Crystal structure of a new heat-labile enterotoxin, LT-IIb.";
Structure 4:665-678(1996).

Comments

- ***FUNCTION***: The biological activity of the toxin is produced by the A chain, which activates intracellular adenyl cyclase.
- ***SUBUNIT***: Heterohexamer of one A chain and of five B chains.

Copyright

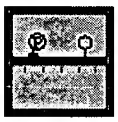
Cross-references

EMBL	M28523; AAA53286.1; -; [EMBL / GenBank / DDBJ] Genomic_DNA. [CoDingSequence]
PIR	B33959; B33959.
PDB	1QB5; X-ray; D/E/F/G/H=24-122. [ExPASy / RCSB / EBI] 1QCB; X-ray; D/E/F/G/H=24-122. [ExPASy / RCSB / EBI] 1TII; X-ray; D/E/F/G/H=24-122. [ExPASy / RCSB / EBI] Detailed list of linked structures.
InterPro	IPR010503; LT-IIB. Graphical view of domain structure.
Pfam	PF06453; LT-IIB; 1. Pfam graphical view of domain structure.
ProDom	PD031532; LT-IIB; 1. [Domain structure / List of seq. sharing at least 1 domain]
HOGENOM	[Family / Alignment / Tree]
BLOCKS	P43529.
ProtoNet	P43529.
ProtoMap	P43529.
PRESAGE	P43529.
DIP	P43529.
ModBase	P43529.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

3D-structure; Enterotoxin; Signal; Toxin.

Features


Feature table viewer

Key	From	To	Length	Description	FTId
SIGNAL	1	23	23		
CHAIN	24	122	99	Heat-labile enterotoxin IIB, B chain.	PRO_0000019358
DISULFID	33	104			
HELIX	27	33	7		
TURN	34	35	2		
STRAND	39	44	6		
STRAND	46	52	7		
TURN	55	57	3		
STRAND	59	64	6		
TURN	65	66	2		
STRAND	69	72	4		
TURN	78	79	2		
HELIX	80	97	18		
STRAND	101	106	6		
TURN	107	108	2		
STRAND	112	120	9		

Sequence information

Length: **122 AA** [This is the length of the unprocessed precursor]

Molecular weight: **13255 Da** [This is the MW of the unprocessed precursor]

CRC64: **308A6CE5F0CFD494** [This is a checksum on the sequence]

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MSFKKIIKAF VIMAALVSVQ AHAGASQFFK DNCNRTTASL VEGVELTKYI SDINNNTDGM

        70         80         90        100        110        120
YVVSSTGGVW RISRAKDYPD NVMTAEMRKI AMAAVLSGMR VNMCASPASS PNVIWAIELE

AE
```

P43529 in FASTA format

View entry in original UniProtKB/Swiss-Prot format
View entry in raw text format (no links)
Report form for errors/updates in this UniProtKB/Swiss-Prot entry

BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-MODEL

NPSA Sequence analysis tools

UniProtKB/Swiss-Prot entry P01555

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**CHTA_VIBCH**
Primary accession number	**P01555**
Secondary accession numbers	Q56634 Q9JPV1
Entered in Swiss-Prot in	Release 01, July 1986
Sequence was last modified in	Release 02, October 1986
Annotations were last modified in	Release 49, January 2006

Name and origin of the protein

Protein name	**Cholera enterotoxin, A chain [Precursor]**
Synonyms	**NAD(+)--diphthamide ADP-ribosyltransferase** **EC 2.4.2.36**
Contains	**Cholera enterotoxin A subunit** **Cholera enterotoxin subunit A1** (Cholera enterotoxin A1 chain) (Cholera enterotoxin alpha chain) **Cholera enterotoxin subunit A2** (Cholera enterotoxin A2 chain) (Cholera enterotoxin gamma chain)
Gene name	**Name: ctxA** Synonyms: toxA OrderedLocusNames: VC1457
From	Vibrio cholerae [TaxID: 666]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=El Tor 2125;
PubMed=6646234 [NCBI, ExPASy, EBI, Israel, Japan]
Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F., de Wilde M.;
"Cholera toxin genes: nucleotide sequence, deletion analysis and vaccine development.";
Nature 306:551-557(1983).

[2] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=Classical 569B / ATCC 25870 / Serotype O1;
DOI=10.1016/0167-4781(91)90050-V; PubMed=1883840 [NCBI, ExPASy, EBI, Israel, Japan]
Dams E., de Wolf M., Dierick W.;
"Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classical strain 569B.";

Biochim. Biophys. Acta 1090:139-141(1991).

[3] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=1854 / O139-Bengal;
Yamamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J., Honda T.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=El Tor 2125;
Dams E., de Wolf M., Dierick W.;
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.

[5] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=KNIH002;
Shin H.J., Park Y.C., Kim Y.C.;
"Cloning and nucleotide sequence analysis of the virulence gene cassette from Vibrio cholerae KNIH002 isolated in Korea.";
Misainmurhag Hoiji 35:205-210(1999).

[6] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=El Tor N16961 / Serotype O1;
DOI=10.1038/35020000; PubMed=10952301 [NCBI, ExPASy, EBI, Israel, Japan]
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L., Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., [redacted], Fraser C.M.;
"DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
Nature 406:477-483(2000).

[7] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-212.
STRAIN=Classical 569B / ATCC 25870 / Serotype O1;
PubMed=6090390 [NCBI, ExPASy, EBI, Israel, Japan]
Lockman H.A., Galen J.E., Kaper J.B.;
"Vibrio cholerae enterotoxin genes: nucleotide sequence analysis of DNA encoding ADP-ribosyltransferase.";
J. Bacteriol. 159:1086-1089(1984).

[8] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 213-258.
PubMed=6315707 [NCBI, ExPASy, EBI, Israel, Japan]
Lockman H., Kaper J.B.;
"Nucleotide sequence analysis of the A2 and B subunits of Vibrio cholerae enterotoxin.";
J. Biol. Chem. 258:13722-13726(1983).

[9] PROTEIN SEQUENCE OF 19-27.
DOI=10.1016/0014-5793(81)80238-4; PubMed=7238869 [NCBI, ExPASy, EBI, Israel, Japan]
Duffy L.K., Peterson J.W., Kurosky A.;
"Isolation and characterization of a precursor form of the 'A' subunit of cholera toxin.";
FEBS Lett. 126:187-190(1981).

[10] PROTEIN SEQUENCE OF 19-38 AND 213-232.
DOI=10.1016/0019-2791(76)90173-7; PubMed=955672 [NCBI, ExPASy, EBI, Israel, Japan]
Klapper D.G., Finkelstein R.A., Capra J.D.;
"Subunit structure and N-terminal amino acid sequence of the three chains of cholera enterotoxin.";
Immunochemistry 13:605-611(1976).

[11] PROTEIN SEQUENCE OF 27-72 AND 111-139.
DOI=10.1016/0014-5793(79)81136-9; PubMed=437113 [NCBI, ExPASy, EBI, Israel, Japan]
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Comments

- ***FUNCTION***: The A1 chain catalyzes the ADP-ribosylation of Gs alpha, a GTP-binding regulatory protein, to activate the adenylate cyclase. This leads to an overproduction of cAMP and eventually to a hypersecretion of chloride and bicarbonate followed by water, resulting in the characteristic cholera stool. The A2 chain tethers A1 to the pentameric ring.
- ***CATALYTIC ACTIVITY***: NAD^+ + peptide diphthamide = nicotinamide + peptide N-(ADP-D-ribosyl)diphthamide.
- ***SUBUNIT***: The holotoxin (choleragen) consists of a pentameric ring of B subunits whose central pore is occupied by the A subunit. The A subunit contains two chains, A1 and A2, linked by a disulfide bridge.
- ***DOMAIN***: The four C-terminal residues of the A2 chain occupy the central pore of the holotoxin. Deletion of this residues weakens the interaction between the A subunit and the B pentamer whithout impairing the pentamer formation.
- ***MISCELLANEOUS***: After binding to gangliosides GM1 in lipid rafts, through the subunit B pentamer, the holotoxin and the gangliosides are internalized. The holotoxin remains bound to GM1 until arrival in the ER. The A subunit has previously been cleaved in the intestinal lumen but the A1 and A2 chains have remained associated. In the ER, the A subunit disulfide bridge is reduced, the A1 chain is unfolded by the PDI and disassembled from the rest of the toxin. Then, the membrane-associated ER oxidase ERO1 oxidizes PDI, which releases the unfolded A1 chain.

The next step is the retro-translocation of A1 into the cytosol. This might be mediated by the protein-conducting pore SEC61. Upon arrival in the cytosol, A1 refolds and avoids proteasome degradation. In one way or another, A1 finally reaches its target and induces toxicity.

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Cross-references

EMBL	X00171; CAA24995.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	X58785; CAA41590.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	D30053; BAA06290.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	X58786; CAA41592.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	K02679; AAA27514.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF175708; AAD51359.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AE004224; AAF94614.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	K01170; AAA27572.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	D30052; BAA06288.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A05129; XVVCA.	
PDB	1S5B; X-ray; A=19-258.	[ExPASy / RCSB / EBI]
	1S5C; X-ray; A=19-258.	[ExPASy / RCSB / EBI]
	1S5D; X-ray; A=19-258.	[ExPASy / RCSB / EBI]
	1S5E; X-ray; A/B=19-258.	[ExPASy / RCSB / EBI]
	1S5F; X-ray; A=19-258.	[ExPASy / RCSB / EBI]
	1XTC; X-ray; A=19-212, C=213-258.	[ExPASy / RCSB / EBI]
	Detailed list of linked structures.	
TIGR	VC1457; -.	
InterPro	IPR001144; Enterotoxin_A. Graphical view of domain structure.	
Pfam	PF01375; Enterotoxin_a; 1. Pfam graphical view of domain structure.	
PRINTS	PR00771; ENTEROTOXINA.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOGENOM	[Family / Alignment / Tree]	
BLOCKS	P01555.	
ProtoNet	P01555.	
ProtoMap	P01555.	
PRESAGE	P01555.	
DIP	P01555.	
ModBase	P01555.	

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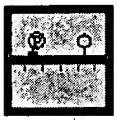
UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

3D-structure; Complete proteome; Direct protein sequencing; Enterotoxin; Glycosyltransferase; NAD; Signal; Toxin; Transferase.

Features

 Feature table viewer

 Feature aligner

Key	From	To	Length	Description	FTId
SIGNAL	1	18	18		
CHAIN	19	212	194	Cholera enterotoxin subunit A1.	PRO_0000019342
CHAIN	213	258	46	Cholera enterotoxin subunit A2.	PRO_0000019343
ACT_SITE	130	130		*By similarity.*	
BINDING	25	25		NAD *(By similarity).*	
BINDING	62	62		NAD *(By similarity).*	
DISULFID	205	217		Interchain (between A1 and A2 chains).	
CONFLICT	20	20		D -> N (in Ref. 9).	
CONFLICT	37	37		S -> R (in Ref. 10).	
CONFLICT	39	39		G -> L (in Ref. 11).	
CONFLICT	45	46		QS -> SE (in Ref. 11).	
CONFLICT	111	111		N -> L (in Ref. 11).	
CONFLICT	132	132		S -> A (in Ref. 11).	
CONFLICT	213	213		M -> I (in Ref. 1).	
CONFLICT	247	248		DI -> ID (in Ref. 12).	
CONFLICT	256	256		D -> N (in Ref. 12).	
STRAND	24	27	4		
HELIX	31	37	7		
TURN	38	38	1		
STRAND	39	40	2		
TURN	43	44	2		
TURN	48	49	2		
HELIX	59	63	5		
TURN	64	64	1		
TURN	75	76	2		
STRAND	77	81	5		
HELIX	85	89	5		
TURN	90	91	2		
TURN	96	97	2		
STRAND	101	106	6		
TURN	110	111	2		
STRAND	112	114	3		
HELIX	115	119	5		
HELIX	120	122	3		
HELIX	126	128	3		
STRAND	130	134	5		

STRAND	137	138	2
TURN	139	141	3
STRAND	142	148	7
STRAND	153	159	7
TURN	161	162	2
HELIX	165	168	4
TURN	169	170	2
HELIX	176	178	3
TURN	187	188	2
HELIX	190	193	4
TURN	195	196	2
HELIX	197	199	3
TURN	200	200	1
TURN	203	204	2
HELIX	215	251	37
TURN	252	253	2
HELIX	254	258	5

Sequence information

Length: **258 AA** [This is the length of the unprocessed precursor]

Molecular weight: **29336 Da** [This is the MW of the unprocessed precursor]

CRC64: **0F7EBAE62069A5D0** [This is a checksum on the sequence]

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        10         20         30         40         50         60
MVKIIFVFFI FLSSFSYAND DKLYRADSRP PDEIKQSGGL MPRGQSEYFD RGTQMNINLY

        70         80         90        100        110        120
DHARGTQTGF VRHDDGYVST SISLRSAHLV GQTILSGHST YYIYVIATAP NMFNVNDVLG

       130        140        150        160        170        180
AYSPHPDEQE VSALGGIPYS QIYGWYRVHF GVLDEQLHRN RGYRDRYYSN LDIAPAADGY

       190        200        210        220        230        240
GLAGFPPEHR AWREEPWIHH APPGCGNAPR SSMSNTCDEK TQSLGVKFLD EYQSKVKRQI

       250
FSGYQSDIDT HNRIKDEL
```

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BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-MODEL

NPSA Sequence analysis tools